

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/407,806

DATE: 11/03/1999
 TIME: 13:58:51

INPUT SET: S33828.raw

**This Raw Listing contains the General
 Information Section and up to the first 5 pages.**

1
 2
 3 (1) General Information
 4
 5 (i) APPLICANT: Murphy, Dennis
 6 Reid, John
 7
 8 (ii) TITLE OF THE INVENTION: ALPHA-GALACTOSIDASE
 9
 10 (iii) NUMBER OF SEQUENCES: 4
 11
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Fish & Richardson, P.C.
 14 (B) STREET: 4225 Executive Square, Suite 1400
 15 (C) CITY: La Jolla
 16 (D) STATE: CA
 17 (E) COUNTRY: US
 18 (F) ZIP: 92037
 19
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette
 22 (B) COMPUTER: IBM Compatible
 23 (C) OPERATING SYSTEM: Windows95
 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 25
 26 (vi) CURRENT APPLICATION DATA:
 27 (A) APPLICATION NUMBER: 09/407,806
 28 (B) FILING DATE:
 29 (C) CLASSIFICATION:
 30
 31 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: 08/613,220
 33 (B) FILING DATE:
 34
 35 (viii) ATTORNEY/AGENT INFORMATION:
 36 (A) NAME: Haile, Ph.D., Lisa A.
 37 (B) REGISTRATION NUMBER: 38,347
 38 (C) REFERENCE/DOCKET NUMBER: 09010/004001
 39
 40 (ix) TELECOMMUNICATION INFORMATION:
 41 (A) TELEPHONE: 619-678-5070
 42 (B) TELEFAX: 619-68-5099
 43 (C) TELEX:
 44
 45 (2) INFORMATION FOR SEQ ID NO:1:
 46

ENTERED

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 52 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: single
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57      CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAGAGCG CTCGTCTTTC AC      52
58
59      (2) INFORMATION FOR SEQ ID NO:2:
60
61      (i) SEQUENCE CHARACTERISTICS:
62          (A) LENGTH: 31 base pairs
63          (B) TYPE: nucleic acid
64          (C) STRANDEDNESS: single
65          (D) TOPOLOGY: linear
66
67      (ii) MOLECULE TYPE: cDNA
68
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71      CGGAAGATCT AGGTTCCCA TTTTCACCCC T      31
72
73      (2) INFORMATION FOR SEQ ID NO:3:
74
75      (i) SEQUENCE CHARACTERISTICS:
76          (A) LENGTH: 1041 base pairs
77          (B) TYPE: nucleic acid
78          (C) STRANDEDNESS: single
79          (D) TOPOLOGY: linear
80
81      (ix) FEATURE:
82          (A) NAME/KEY: Coding Sequence
83          (B) LOCATION: 1...1038
84          (D) OTHER INFORMATION:
85
86      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
87
88      TTG AGA GCG CTC GTC TTT CAC GGC AAC CTC CAG TAT GCC GAA ATC CCA      48
89      Leu Arg Ala Leu Val Phe His Gly Asn Leu Gln Tyr Ala Glu Ile Pro
90      1          5          10          15
91
92      AAG AGC GAA CCA AAG GTC ATA GAG AAG GCA TAC ATC CCA GTC ATC GAG      96
93      Lys Ser Glu Pro Lys Val Ile Glu Lys Ala Tyr Ile Pro Val Ile Glu
94      20          25          30
95
96      ACA CTG ATT AAA GAA GAA CCT TTT GGG CTC AAC ATA ACG GGC TAT ACC      144
97      Thr Leu Ile Lys Glu Glu Pro Phe Gly Leu Asn Ile Thr Gly Tyr Thr
98      35          40          45
99

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100	TTA AAG TTC CTC CCG AAG GAT ATT ATA CTC GTT AAA GGG GGC ATC GCG	192
101	Leu Lys Phe Leu Pro Lys Asp Ile Ile Leu Val Lys Gly Gly Ile Ala	
102	50 55 60	
103		
104	AGT GAC CTG ATA GAG ATA ATC GGA ACG AGC TAC ACG GCA ATA CTC CCC	240
105	Ser Asp Leu Ile Glu Ile Ile Gly Thr Ser Tyr Thr Ala Ile Leu Pro	
106	65 70 75 80	
107		
108	CTC CTG CCG CTT AGC AGA GTA GAA GCA CAA GTT CAG AGA GAT AGG GTT	288
109	Leu Leu Pro Leu Ser Arg Val Glu Ala Gln Val Gln Arg Asp Arg Val	
110	85 90 95	
111		
112	AAG GAA GAG CTC TTC GAG GTT TCT CCA AAG GGA TTC TGG CTG CCA GAG	336
113	Lys Glu Glu Leu Phe Glu Val Ser Pro Lys Gly Phe Trp Leu Pro Glu	
114	100 105 110	
115		
116	CTC GCC GAC CCG ATA ATC CCT GCC ATA CTG AAG GAC AAC GGT TAT GAG	384
117	Leu Ala Asp Pro Ile Ile Pro Ala Ile Leu Lys Asp Asn Gly Tyr Glu	
118	115 120 125	
119		
120	TAT CTA TTC GCC GAC GAG GCG ATG CTT TTC TCA GCT CAT CTC AAC TCG	432
121	Tyr Leu Phe Ala Asp Glu Ala Met Leu Phe Ser Ala His Leu Asn Ser	
122	130 135 140	
123		
124	GCG ATA AAG CCA ATT AAA CCG CTC CCA CAC CTT ATA AAG GCC CAA AGG	480
125	Ala Ile Lys Pro Ile Lys Pro Leu Pro His Leu Ile Lys Ala Gln Arg	
126	145 150 155 160	
127		
128	GAA AAG CGC TTT AGG TAC ATC AGC TAT CTC CTT CTC AGG GAG CTT AGG	528
129	Glu Lys Arg Phe Arg Tyr Ile Ser Tyr Leu Leu Leu Arg Glu Leu Arg	
130	165 170 175	
131		
132	AAG GCG ATA AAG CTC GTT TTT GAA GGT AAG GTA ACG CTA AAG GTC AAA	576
133	Lys Ala Ile Lys Leu Val Phe Glu Gly Lys Val Thr Leu Lys Val Lys	
134	180 185 190	
135		
136	GAC ATC GAA GCC GTA CCC GTT TGG GTG GCC GTG AAC ACG GCT GTA ATG	624
137	Asp Ile Glu Ala Val Pro Val Trp Val Ala Val Asn Thr Ala Val Met	
138	195 200 205	
139		
140	CTC ATC GGA AGG CTT CCT CTT ATG AAT CCT AAG AAA GTG GCG AGC TGG	672
141	Leu Ile Gly Arg Leu Pro Leu Met Asn Pro Lys Lys Val Ala Ser Trp	
142	210 215 220	
143		
144	ATA GAG GAC AAG AAC ATT CTT CTA TAC GGC ACC GAT ATA GAG TTC ATT	720
145	Ile Glu Asp Lys Asn Ile Leu Leu Tyr Gly Thr Asp Ile Glu Phe Ile	
146	225 230 235 240	
147		
148	GGC TAT AGG GAC ATT GCA GGC AGA ATG AGT GTT GAG GGA TTA TTA GAG	768
149	Gly Tyr Arg Asp Ile Ala Gly Arg Met Ser Val Glu Gly Leu Leu Glu	
150	245 250 255	
151		
152	GTT ATA GAC GAG CTC AAC TCG GAA CTG TGC CCC TCA GAG CTG AAG CAC	816

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153 Val Ile Asp Glu Leu Asn Ser Glu Leu Cys Pro Ser Glu Leu Lys His
154      260      265      270
155
156 AGT GGA AGG GAG CTC TAC TTA CGG ACT TCG AGT TGG GCA GAT AAG AGC      864
157 Ser Gly Arg Glu Leu Tyr Leu Arg Thr Ser Ser Trp Ala Asp Lys Ser
158      275      280      285
159
160 TTG AGG ATA TGG AGA GAG GAC GAA GGG AAC GCA AGA CTT AAT ATG CTG      912
161 Leu Arg Ile Trp Arg Glu Asp Glu Gly Asn Ala Arg Leu Asn Met Leu
162      290      295      300
163
164 TAC AAT ATG AGG GGC GAA CTC GCC TTT TTA GCC GAG AAC AGC GAT GCA      960
165 Tyr Asn Met Arg Gly Glu Leu Ala Phe Leu Ala Glu Asn Ser Asp Ala
166      305      310      315      320
167
168 AGG GGA TGG CCC CTC CCT GAG AGG AGG CTG GAT GCC TTC CGG GCG ATA      1008
169 Arg Gly Trp Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Arg Ala Ile
170      325      330      335
171
172 TAT AAC GAT TGG AGG GGT AAT GGG GAA CCT TAG      1041
173 Tyr Asn Asp Trp Arg Gly Asn Gly Glu Pro
174      340      345
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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190 Leu Arg Ala Leu Val Phe His Gly Asn Leu Gln Tyr Ala Glu Ile Pro
191   1       5       10
192 Lys Ser Glu Pro Lys Val Ile Glu Lys Ala Tyr Ile Pro Val Ile Glu
193      20      25      30
194 Thr Leu Ile Lys Glu Glu Pro Phe Gly Leu Asn Ile Thr Gly Tyr Thr
195      35      40      45
196 Leu Lys Phe Leu Pro Lys Asp Ile Ile Leu Val Lys Gly Gly Ile Ala
197      50      55      60
198 Ser Asp Leu Ile Glu Ile Ile Gly Thr Ser Tyr Thr Ala Ile Leu Pro
199      65      70      75      80
200 Leu Leu Pro Leu Ser Arg Val Glu Ala Gln Val Gln Arg Asp Arg Val
201      85      90      95
202 Lys Glu Glu Leu Phe Glu Val Ser Pro Lys Gly Phe Trp Leu Pro Glu
203      100     105     110
204 Leu Ala Asp Pro Ile Ile Pro Ala Ile Leu Lys Asp Asn Gly Tyr Glu
205      115     120     125

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206   Tyr Leu Phe Ala Asp Glu Ala Met Leu Phe Ser Ala His Leu Asn Ser
207       130                      135                      140
208   Ala Ile Lys Pro Ile Lys Pro Leu Pro His Leu Ile Lys Ala Gln Arg
209       145                      150                      155                      160
210   Glu Lys Arg Phe Arg Tyr Ile Ser Tyr Leu Leu Leu Arg Glu Leu Arg
211       165                      170                      175
212   Lys Ala Ile Lys Leu Val Phe Glu Gly Lys Val Thr Leu Lys Val Lys
213       180                      185                      190
214   Asp Ile Glu Ala Val Pro Val Trp Val Ala Val Asn Thr Ala Val Met
215       195                      200                      205
216   Leu Ile Gly Arg Leu Pro Leu Met Asn Pro Lys Lys Val Ala Ser Trp
217       210                      215                      220
218   Ile Glu Asp Lys Asn Ile Leu Leu Tyr Gly Thr Asp Ile Glu Phe Ile
219       225                      230                      235                      240
220   Gly Tyr Arg Asp Ile Ala Gly Arg Met Ser Val Glu Gly Leu Leu Glu
221       245                      250                      255
222   Val Ile Asp Glu Leu Asn Ser Glu Leu Cys Pro Ser Glu Leu Lys His
223       260                      265                      270
224   Ser Gly Arg Glu Leu Tyr Leu Arg Thr Ser Ser Trp Ala Asp Lys Ser
225       275                      280                      285
226   Leu Arg Ile Trp Arg Glu Asp Glu Gly Asn Ala Arg Leu Asn Met Leu
227       290                      295                      300
228   Tyr Asn Met Arg Gly Glu Leu Ala Phe Leu Ala Glu Asn Ser Asp Ala
229       305                      310                      315                      320
230   Arg Gly Trp Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Arg Ala Ile
231       325                      330                      335
232   Tyr Asn Asp Trp Arg Gly Asn Gly Glu Pro
233       340                      345
234
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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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INPUT SET: S33828.raw

< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
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DATE: 11/03/1999
TIME: 13:58:53

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Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
8	(ii) TITLE OF THE INVENTION: ALPHA-GALACTOSID	(ii) TITLE OF INVENTION: ALPHA-GALACTOSIDASE